REMARKS

In the present communication, Claims 13, 16, 18, 19, 22, 30, 31, and 34 have been amended, and Claim 29 has been cancelled. As such, Claims 13, 15-20, 22-25, and 30-45 are currently pending. The Examiner's objections and rejections are as follows:

I) The Examiner objected to the claims and specification for various informalities;

II) The Examiner objected to the specification for containing unlabeled sequences and a hyperlink;

III) The Examiner rejected Claims 16-17 and 19 under 35 U.S.C. 112, second paragraph, as allegedly indefinite;

IV) The Examiner rejected Claims 22-25 under 35 U.S.C. 102(b) as allegedly anticipated by Gattermann et al.;

V) The Examiner rejected Claim 22 under 35 U.S.C. 102(b) as allegedly anticipated by Crespillo et al.; and

VI) The Examiner rejected Claims 13, 15-17, 19-20, 29-37, and 39-45 under 35 U.S.C. 103(a) over Gatterman et al. in view of Crespillo et al. and Aserud et al.

I. Informalities

The Examiner objected to certain claims and the specification. In particular, the Examiner objected to Claims 16-19 as dependent on cancelled claims. These claims have been amended to correct this informality. The Examiner also objected to Figures 20A and 20B for failing to provide SEQ ID NOs. for the sequences in these figures. Applicants have amended the Description of the Figures for Figures 20A and 20B to provide the SEQ ID NOs.

II. Objection to the Specification

The Examiner objected to the specification for two reasons. First, the Examiner objected to the sequences listed in Figures 20A and 20B for failing to be labeled and for failing to be part of the sequence listing. As noted above, the Description of the Figures has been amended to provide the SEQ IDs for these two figures. Also submitted with this communication is a replacement sequence listing (in paper copy and floppy disk) that provides the sequences in these

two figures. The Examiner also objected to the hyperlink on page 25 of the specification. The specification has been amended to delete this hyperlink.

III. Indefiniteness Rejection

The Examiner rejected Claims 16-17 and 19 under 35 U.S.C. 112, second paragraph, as allegedly indefinite for being dependent on cancelled claims. As noted above, these claims have been amended to correct this informality.

IV-V. Anticipation Rejections

The Examiner issued two different anticipation rejections, including a rejection of Claims 22-25 as allegedly anticipated by Gatterman et al. and a rejection of Claim 22 as allegedly anticipated by Crespillo et al. While Applicants disagree with these rejections, for business reasons and to further the prosecution of the present application, without acquiescing to the Examiner's rejection, and while reserving the right to present the original or similar claims in other applications, Applicants have amended the claims. In particular, Claim 22 has been amended to recite the molecular mass of said amplification products is determined by "mass spectrometry, without sequencing said plurality of amplification product." Neither Gatterman et al. (which describes the use of gel electrophoresis) nor Crespillo et al. (which employs sequencing without mass spectrometry) describe or suggest the use of mass spectrometry to determine the mass of the mitochondrial DNA amplification product. Moreover, Crespillo et al. relies on sequencing, as the database in this reference is a sequence based database and the comparison method is based on sequence alignment. As such, Applicants respectfully submit these rejections should be withdrawn.

V. Obviousness Rejection

The Examiner rejected Claims 13, 15-17, 19-20, 29-37, and 39-45 under 35 U.S.C. 103(a) over Gatterman et al. in view of Crespillo et al. and Aserud et al. Applicants respectfully disagree with this rejection and submit that the Examiner has not established a *prima facie* case of obviousness.

As part of this rejection, the Examiner asserts:

> It would have been prima facie obvious to a person of ordinary skill in the art at the time the invention was made to modify the method of mtDNA analysis as taught by Gatterman et al. in a manner as taught by Crespillo et al. by incorporating a mtDNA database comprising known molecular masses and as taught by Aaserud et al. by incorporating measuring base-composition by mass spectrometry for the purpose of enhancing sensitivity of the method for analyzing sequence variation in said target nucleic acid. (*emphasis added*, Office Action page 8).

Thus, the Examiner's motivation for the combination is based on an alleged enhancement of sensitivity.

Applicants respectfully submit that one of ordinary skill in the art would not be motivated to combine the references as suggested by the Examiner for "enhancing sensitivity." The Crespillo et al. reference employs *sequencing*. Applicants submit that one of skill in the art who possessed sequenced amplicons would not be motivated to apply another or different technique (e.g., mass spectrometry) to already sequenced amplicons as applying such additional or alternative technique would not provide *enhanced* sensitivity. In other words, since sequencing not only provides the number of each type of base in an amplicon, but also indicates the exact order of the bases, running an additional or different technique such as mass spectrometry would not provide additional sensitivity. Likewise, the Examiner has not presented any evidence that a skilled artisan would substitute mass spectrometry analysis for the analysis used by Gatterman et al. or Crespillo et al. or that such a substitution would provide an enhancement in sensitivity (e.g., the cited references do not make a sensitivity comparison between these technologies).

Nonetheless, for business reasons and to further the prosecution of the present application, without acquiescing to the Examiner's rejection, and while reserving the right to present the original or similar claims in other applications, Applicants have amended the claims. In particular, Claims 13, 22, and 34 have been amended to recite that the molecular mass of the restriction fragments or amplicons is performed "without sequencing." Applicants note that the database the Examiner is relying on as part of the rejection comes from Caspillo et al., which is a *sequencing* based database (not a molecular weight database). In Caspillo et al. the *sequence* of the fragments are compared to a reference *sequence* using SeqEd V. 1.0.3 (See page 130, col. 2, last sentence). As the present claims have been amended to recite "without sequencing," the

Examiner's combination does not provide all of the elements of the claimed invention because the combination necessarily requires a sequence determination and comparison of linear sequences. Additionally, as the amended claims do not employ sequencing, one of skill in the art could not be motivated to employ the sequence based database and alignment methods of Caspillo et al. As such, Applicants respectfully request that the rejection be withdrawn.

CONCLUSION

Applicants believe that the arguments and claim amendments set forth above traverse the Examiner's rejections and, therefore, request that all grounds for rejection be withdrawn for the reasons set forth above. Should the Examiner believe that a telephone interview would aid in the prosecution of this application, the Applicants encourage the Examiner to call the undersigned collect at 608-218-6900.

Dated: November 3, 2006

Jason R. Bond
Registration No. 45,439

MEDLEN & CARROLL, LLP
101 Howard Street, Suite 350
San Francisco, California 94105
608.218.6900